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June 3, 2003, 15:04:33; Search time 18 Seconds (Without alignments) 1276,451 Million cell updates/sec
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1 1744
1 1745 GEBLFTGVVPILVELD......VLLGFVTAAGITLGMDELXK 239
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
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283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri:* pir2:* pir3:* PIR_73:* Database :

Pred. Wo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		green-fluorescent	hypothetical prote	leucine-tRNA ligas	ч.	leucyl-tRNA synthe	DNA topoisomerase	iron-sulfur cofact	leucyl-tRNA synthe	DNA-directed DNA p	hypothetical prote	dihydrolipoamide d	S-layer protein pr	protective surface	protective surface	tRNA (uracil-5-)-m	DNA-directed DNA p	inter-alpha-trypsi	cellulase (EC 3.2.	hypothetical prote		hypothetical prote	oligoendopeptidase	imidazoleglycerol-	DNA-directed DNA p	IgA Fc receptor pr	ы	photosystem II chl	hypothetical prote	alpha-amylase homo
SUMMARIES		JQ1514	H72228	н64102	T06586	E82590	D83917	E70390	AC0582	A36028	D71614	140794	JC4930	JC4078	F64102	681355	JDVLHH	JC5576	529043	AD2052	JH0414	C97354	A99552	E84941	JDVLD	A60234	FCSOAG	T06936	T27856	T39539
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8 Query Match			8.3	7.2	7.1	7.0	6.9	6.9	•	6.9	•	8.9	6.8	8.9	6.8	9.9	6.7	6.7			6.7	9,6					9.9			6.5
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82.5 82.5 82.5 82.8 82.8 81.5 81.5 81.5	81 80.5
0.0000000000000000000000000000000000000	444

ALIGNMENTS

RESULT 1 GOTO 12 TO 12 T
A.Residues, 46.64;74-122:132-151;154-183;185-200 <pra3> R.Inouve, 5.; Tsuji, F.L. FERSI Lett. 31, 211-214, 1994 A.Title: Evidence for redox forms of the Aequorea green fluorescent protein. A.Reference number: 848693; MGID:94364470; PMID:8082767 A.Accession.; 848693; 848693; MGID:94364470; PMID:8082767</pra3>
A.Rodscule (type: mRN; 4.7, 26.156, 'P', 158-171, 'K', 173-238 <ino> A.Cross references; GSL129445; NID:9606383; PIDN:AA58246.1; PID:9606384 A.Rodstules, J. N.; Campbell, A. R. Romstell, Data Library, January 1995 A.Rocesion: SS1330 A.Rocesion: SS1330 A.Rodesiules; SS1330 A.Rodesiule: Liprary, A.Rodesiule: A.Rodstolle (type: mRN; A.Rodstoll</ino>
A/Experimental source clone gfpl A. Accession: 55131 A. Molecule type: mark A. M. M. A.

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NAItenate names laucyl-trikk synthetase to the state that it is a state to the state of the state to the state of the state to the state of the state of
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"Description: identification of a novel family of DNA-binding proteins with two An-A.Reference number: 215774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD----- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 TGDKLPI-WVANFVLMHYGTGAVMAVPAH-DQRDF-----EFAQKYSLPIKQVIAPLA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 DEBIDLTRQAFVEHGKLVNSDEFDGKNF--DGAFNG------IADKLEKLGV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 IVDQGRDVDGSKVDVINKESNEATIPENK----PTEPKLDVEQELAATIM------ 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. Nat.binding procein PDZ - garden pea
C.Species: Plsum sativum (garden pea)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
S.Sato, N.; Razuno, A.A.; Ohte, N.; Ohshima, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 DGNYKTRAEVKFEGDTLVNRIELKGIDFREDGNILGHKLEYNYNSHNVYIMADK-QKNGI
                                                                                                                                      Leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
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A; Residues: 1-632 <SATD.
A; Cross = references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
A; Experimental source: cv. Alaska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: leuS
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein blosynthesis
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23.3%; Pred. No. 12;
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A.Status: praliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
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7.2%; Score 91.5; Di
Best Local Similarity 24.1%; Pred. No. 13;
Matches 46; Conservative 26; Mismatches
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Best Local Similarity
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A:Contents: annotation: X-ray crystallography, 1.9 angstroms
C:Comment: This protein is scrited by the photoprotein aggorin (see PIR:AOJFWV) emittin
C:Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Accession: H72228
A:Stetus: pre-liminary
A:Notacus of type: DNA
A:Residues: 1-785 - CARN>
A:Residues: 1-785 - CARN>
A:Residues: 1-785 - CARN>
A:Cross-references: GB:AR001806; GB:AR000512; NID:g4982196; PIDN:AAD36691.1; PID:g498219
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A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A.Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 NRIELKGIDFKEDGNILGHKLEYNYNSHNYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 TTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Thermotoga maritima
C:Abte: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: H72228
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                                                                                                                                                                                            **. Introns. 7 69/3; 167/3

**. Introns. 7 green-fluorescent protein
C. Superfamily: green-fluorescent protein
C. Keywords: chromoprocein; luminescence
C. Keywords: chromoprocein; luminescence
C. Keywords: chromoprocein; luminescence
C. Keywords: chromoprocein; luminescence
C. Status experimental
F: 66/wooditied site: debydrocyrosine (Tyr) featus experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 97.4%; Score 1241; DB 1; Length 238; Local Similarity 97.1%; Pred. No. 0.3e-97; Pred. Score 13e. 23i; Conservative 4; Mismatches 3; Indels nes 23i; Conservative 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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RyTakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A; Fithe: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A; Reference number: R83550; MUID:20512582; FMID:11058132
A; Accession: D83917
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Natches 53; Conserv
                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-655 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN00:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 TTGKLPVPWPTLVTTLSYGVQCPSRYPDHMKQRDFFKSAMPEG¥VQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 ......KTRAEVKFEGDTLVNRIELKGIDFKEDQNILGHKLEYNYNSHNYYI 153
                                                                                                                             -----YNYNSHNVYIMADKQK-----N 160
                                                                                                                                                                          PSSAKVNVLTKDLIVETFPLRSVARTSSGREGSEELKDSGNSLERDTKKLELEQGKNS-E 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leucyl-tRNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c)
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22.2%; Pred. No. 20;
tive 29; Mismatches
                                                                                                                                                                                                                                                                                            161 GIKVNFKIRHNIEDG-----SVQLADHYQ 184
                                                                                                                                                                                                                                                                                                                                               LKGIDFKEDGNILGHKLE-----
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A; Molecule type: DNA
A; Residues: 1-887 <SIM>
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R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E
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A.Residues: 1.370 "AQP>
A.Residues: 1.370 "AQP>
A.Residues: 1.370 "AQP>
A.Residues: 1.370 "ADPOINTED NID:92983529; PIDN:AAC07111.1; PID:92983536; GB:AA.Reportmental source: strain VFS
A.Cross-references: GB:AP001514; GB:BA000004; NID:q10174613; PIDN:BAB05859.1; GSPDB
A/Experimental source: strain C-125
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A,Recession: E70390
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                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER-----TIFFKDDG----- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 SVVNALSEWLIVEIKRDGWVYEORFENGGKPSTTLEKKGKTROTGTTIHFRPDPTVFSTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----QKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 VFFNGESNGIEIEFAFOFN--DGYTENVLSFVNNVRTKDG-----GTHELGAKTAMTRAV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Superfamily: nitrogen fixation protein nifs
C;Rewpords: phosphoprotein: pyridoxal phosphate; sulfurtransferase
F;195/Antining site: pyridoxal phosphate (Lys) (covalent) #status predicted
F;318/Antine site: Cys (cysteine persulfide intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iron-sulfur cofactor synthesis protein nifs - Aquifex acolicus
Nicontains: L-cystene sulfurtransferase (BC 2.8.1.-)
Cispecies: Aquifex acolicus
Cispecies: Aquifex acolicus
Cispecies: Resquence_revision 08-May-1998 *text_change 07-Dec-1999
Cispecies: B70390
                                                                                                                                                                                                                                                                                                                                                                                              63 NVTIHKDQSVSVRDEGRGMPTGMHKLGKPTPEVILTVLHAGGKFGQGGYATSGGLHGVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 --NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-----
                                                                                                                                                                                                                                                                                                                                         -----CTTGKLPVPWP
                                                                                                                                                                                                                                                                       57;
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C;Buperfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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                                                                                                                                                                                                              DB 2;
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25.4%; Pred. No. 9.5;
:ive 30; Mismatches
                                                                                                                                                                                                     6.9%; Score 88.5; DE
ilarity 21.9%; Pred. No. 17;
Conservative 37; Mismatches
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A/Nolecule type: DNA
A/Residues: 1-2573 CAR>
A/Cross-references: GB:AE001396; GB:AE001362; NID:g3845188; PIDN:AAC71881.1; PID:g388
C;Genetics:
                                                                                                                                                                                                                                                  A.Residues: 1-221 <5EF-
A.Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
A.Note: the nuclectide sequence was submitted to the EMBL Data Library, October 199°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A:Reterence number: 7/1600; WUID:99021743; PMID:9804551
A:Accession: D/1614
                                                                                                                                                                                                                                                                                                                                                                                                R.Schr.Gatta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
A.fitle: The sequence of a 24 152 bp segment from the left arm of chromosome XIV
A.Reference number: S65111; MUID:96310631; PMID:8740425
A.Accessjon: S65121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 VQERTIFFKD--DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN--YNSH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 LPVPWP-TLVTTLSYGVQCFSRYPDHM-----KQHDFFKSAMPEGYV---QERTI 99
                                                      A.Molecule type: DNA
Residues: 1-222 (SEBN>
A.Cross-references: NBB: X92494; NID:g1045236, PIDN:CAA63235.1; PID:g1045247
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                                                                                                                                                  N.; Hegemann, J.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Mop position: 14L
C.Superfamily: DM-directed DNA polymerase II
C.Feyvords: DNA binding; nucleotidyltransferase; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: nucleic acid sequence not shown; translation not shown A.Molecule \mathbf{type}: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 6.9%; Score 87.5; DB 1
Best Local Similarity 28.2%; Pred. No. 1e+0:
Maches 7; Conservative 14; Mismatches 4
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26.2%; Pred. No. 1....
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A;Cross-references: SGD:S0005206; MIPS:YNL262w
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Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 S--HNVYIMAD 156
A; Reference number: S60909
A; Accession: S60919
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A; Molecule type: protein
A; Medidues: 1214-1216, 77, 1218-1221 <MO2>
A; Medidues: 1214-1216, 78, 7; Fleig, U.; Middenthal, R.N.; Hegemann, J.M.
Sch-Gupta, M.; Lyck, R.; Fleig, U.; Middenthal, R.N.; Hegemann, J.M.
Submitted to the EMBL Data Library, October 1995
A; Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L. T.; Connarton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mollo, S.; O'Goora, P.
Reture 413, 848-532, 201, A.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A./Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A./Altic: Complete genome sequence of a multiple drug resistant Salmonella enterios serow A./Rieference number: AM3050; PWIN.11677608
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N.Alternate names: DNA-directed DNA polymerase II chain A; protein N0825; protein YML263
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A;Residues: 1-222 <MOR>
A;Cross-references: GB:M60416; GB:M36724; NID:g171408; PIDN:AAA88711.1; PID:g171409
A;Accession: B36028
283 ERSPSISSVIMPKFFGAETVNKLSEKGIYCSTGSACLSGEYEPNKHMLKMGFSQEKALRM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA_
A;Mesidues: 1-860 cpAs.
A;Cross-references: GB:AL513382; PIDN:CAD0$125.1; PID:g16501899; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 SEQALTEKGVLFNSGEPGLAFEAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 H-----STQSALSKDP 212
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                                                                               105 GNYKTRAEV---KFEGDTLVNRIELKGIDFKEDGNILGHRLEYNYNSHNVYIMADKQKNG 161
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C;Date: 10-28p-1399 #sequence_retiste
C;Abte: 10-28p-1399 #sequence_retiste
C;Abte: 10-28p-1399 #sequence_retiste
C;Abtes: 10-28p-1399 #sequence_retiste
C;Abtes: 10-28p-1399 #sequence_retiste
C;Abtes: 10-28p-1399 #sequence_retiste
Call 62, 1143-1151, 1990
A;Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A;Reference number: A36028; MOID:90381771; PAID:2169345
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ilarity 23.3%; Pred. No. 29;
Conservative 21; Mismatches
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                                                                                                                                                                                                                                                                  343 VRFSFGLLNKEEE 355
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Best Local Similarity
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A; Status: preliminary
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Length 874;

--YGKLTLKFI

--NGIKVNFKIRHN---IEDGSVQLADH 182

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C; Comment: This protein is a glycoprotein. It functions as protective coats, molecu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 KEVFPQTGVVKVLDVTTTNEGSIGTSSIKVKGENVGAGTIHFQNPNASGEGYGSLHVEVT 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 TIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID---FKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 669 RV-----GNDKI-ASAKIEGKTLKVTGKTAGVTDVILIKDGATAGH-ATITVTQENIQIT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             722 SVKFKDVEVEQFENRKVNIDRVLDVVKSDKDDVLNGIKLNISTEHKVRIVDEGTEQ---- 777
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                         A;Cross-references; GB:U38842; NID:g1055336; PIDN:AAC44405.1; PID:g1055337
A;Experimental source: strain NM105
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A; Wesldwas: 1.797 <21.7
A; Crossarzeferenes: G8:013961; NID:9537447; PIDN:AAA85645.1; PID:9537448
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C:Superimally: protective surface antigen D-15
F:1-13/Domain: stipmal sequence *status predicted <SIG>
F:10-79/7/Product: protective surface antigen D-15 *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTA 227
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                                                                                                                                                                                                                                                                                                                      F;1-29/Domain: signāl sequence #statús predicted <SIG>
F;0-54/Product: S.layer protein #status predicted <A/AI>
F;57-209/Domain: S.layer repeat homology <SLR3>
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; Pred. No. 32;
30; Mismatches
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Pred. No.
                                                                                                                                                                                                                                         A, Gene: olpA
C, Superfamily: S-layer repeat homology
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A; Residues: 1-874 <ZHU>
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Best Local 8
                                                                                                                                                                                           C; Genetics:
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S. Layer protein precursor - Bacillus licheniformis
S. Layer protein precursor - Bacillus licheniformis
C. Species: Bacillus licheniformis
C. Species: Bacillus licheniformis
C. Species: Bacillus licheniformis
C. Species: Date 1999
S. Marcossion: J. 04930, R.; Malathi, P.; Ghosh, B.K.
Gene 173, 189-194, 1996
A.; Mitcher The complete nucleotide sequence of the Bacillus licheniformis NM105 S-layer-en
A.; Reference number: J. 04930, MUID: 97082965; PMID: 8964497
A.; Molecule type: DNA
A.; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dihydrolipoamide dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum Millernate names: 2-roapolitzate dehydrogenase complex chain E3; acetoin dehydrogenase complex complex chain E3: S-complex 50K chain C; Species: Clostridium magnum magnum magnum magnum magnum c; Species: 10-ept-1999 #sequence_revision 10-sep-1999 #text_change 21-Jul-2000 [5, Accession: 140794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A) Parking acctoin delydrogenase enzyme system c.special delydrogenase c.special delydrogenase enzyme system c.special delydrogenase dilydrollopamide dehydrogenase c.special Alcalidement delydrollopamide dehydrogenase c.special proper family. Alcalidement delydrollopam del dehydrogenase; redox-active disulfide F:15-77 Comain: lppy/Notin-binding homology (LPB) (APP) (APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rikruger, N.; Oppermann, F.B.; Lorenzl, B.; Steinbuchel, A.
J. Bacteriol. 176, 3614-3630, 1994
A. Rateriol. 176, 3614-3630, 1994
A. Reteriol. 140799; MUID:94266715; PMID:8206840
A. Steference number: 140799; MUID:94266715; PMID:8206840
A. Stetus: pre-liminary; translated from GB/BHBL/DDBJ
A. Holecule type: DMA
A. Reteriol. 14799
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LKKETILCKDIKSGSNDPMDEISLFKDDMVDDKELK--DFEKSSLKIKNKEVYNFIYNKM 183
                                                                                                       150 NVYIMADKOKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS 209
                                                                                                                                                                                     184 NIHIKENKKKDEKEKKNKIHNNDENNWA----IYYKNI---DKTHYILDNNVVHILNDIN 236
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C:Function:
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3.5%; Pred. No. 19;
ve 40; Mismatches 84; Indels
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Matches 54; Conservative
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11;

Gaps

63;

78; Indels

DB 2; Length 797;

66

---NTPIGDGPVLL 196

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129 IDFKED-----GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173
                                                                                                                  14 EKHSFIKKYFKEFYTKDFKLFASKOKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY 73
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Job time: 21 secs
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                                                                                                                                                     Protective surface antigen D-15 - Heamophilus influenzae (strain Rd KW20)
C;Species immemophilus influenzae
C;Species immemophilus influenzae
C;Species immemophilus influenzae
C;Species immemophilus influenzae
C;Date: 18-Aug-1936 sequence_revision 18-Aug-1935 stext_change 18-Sep-1936
C;Accession: Fédilo2
F;Cocyane J.D.; Scort, J.; Shilley, R.; Liu, L.I.; Glodek, A.; Kithness, E.F.; Kerlavage, F;Cocyane, J.D.; Scort, J.; Shilley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.C.; Enno, L.D.; Filtehman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, Schence 269, 466-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Frassr, C.M.; Smith, H.O.; Venter, A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Frassr, C.M.; Smith, H.O.; Venter, A;Authors: mucheic acid sequence not shown; translation not shown
A;Status; nucleic acid sequence not shown; translation not shown
A;Status; Lebos A;Ings
A;Coss-references: GB:L42023; TIGR:HI0917
C;Superfamily: protective surface antigen D-15
C;Neywords: surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 86.5; DB 2; Length 808;
llarity 21.9%; Pred. No. 32;
Conservative 30; Mismatches 78; Indels 6
197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
                            197 P--DNHYLSTQSALSKDPNEKRDHMYLLGFVTAAGITLG 233
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Best Local S:
Matches 48;
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C. Accession: G81355

S. Paren, B.W., Mungall, K., Ketley, J.W., Churcher, C., Basham, D.; Chillin K., Paren, B.W., Mungall, K., Ketley, J.W., Churcher, C., Basham, D.; Chillin Kature d. G.W.; Vanvlict, A.; Whitchead, S.; Barrel W., Stature G.W.; Ouall, W.; Ralandream, W.A.; Rutherford, K., Vanvlict, A.; Whitchead, S.; Barrel M.; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf. A. Reference number A81250; WUID:20150912; PMID:10686204 Campylobacter jejuni reveals hyf. A. Accession: G81355
A. Status preliminary
A. McStdues: 1-957 CPAR
A. Richael Campylobacter Jespan
A. Richael Campylobacter Jes
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80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 128

à

Query Match
General Sanitarity 24.0%, Fred, No. 12,
Best Local Sanitarity 24.0%, Fred, No. 12,
Matches 30; Conservative 18, Mismatches 39; Indels

C; Keywords: methyltransferase; S-adenosylmethionine

34; Gaps

tRNN (ureacl.5-)-methyltransferase (EC 2.1.1.35) Cj0831c [imported] - Campylobacter jeju C; Species: Campylobacter jejun. C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002